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WHAT IS CLAIMED IS:

1. A method for producing a motif-specific, context-independent antibody that recognizes a plurality of peptides or proteins within a genome that contain the motif, said method comprising the steps of:

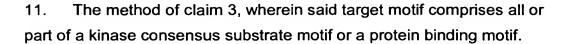
- (a) constructing a degenerate peptide library comprising (i) a fixed target motif comprising one or more invariant amino acids, and (ii) a plurality of degenerate amino acids flanking said motif;
- (b) immunizing a host with said peptide library to raise a context-independent antibody specific for a motif consisting of all or part of said target motif; and
- (c) isolating antisera from said host, and purifying the motifspecific, context-independent antibody of step (b) from said antisera, said antibody recognizing a plurality of peptides or proteins within a genome that contain said motif.
- 2. The method of claim 1, further comprising the step of utilizing spleen cells from the host of step (b) to generate at least one monoclonal, motif-specific, context-independent antibody.
- 3. A method for producing a motif-specific, context-independent antibody that recognizes a plurality of peptides or proteins within a genome that contain the motif, said method comprising the steps of:
 - (a) constructing a degenerate peptide library comprising (i) a fixed target motif comprising one to six invariant amino acids including at least one modified amino acid, and (ii) a plurality of degenerate amino acids flanking said motif;
 - (b) immunizing a host with said peptide library to raise a contextindependent antibody specific for a motif consisting of all or part of said target motif; and

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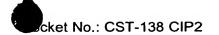
(c) isolating antisera from said host, and purifying the motifspecific, context-independent antibody of step (b) from said antisera, said antibody recognizing a plurality of peptides or proteins within a genome that contain said motif.

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- 4. The method of claim 3, wherein said modified amino acid is selected from the group consisting of a phosphorylated amino acid, an acetylated amino acid, and a nitrosylated amino acid.
- 5. The method of claim 4, wherein said phosphorylated amino acid is selected from the group consisting of phosphothreonine, phosphoserine, and phosphotyrosine.
- 6. The method of claim 4, wherein said acetylated amino acid is acetyl-lysine.
- 7. The method of claim 4, wherein said nitrosylated amino acid is nitrotyrosine.
- 8. The method of claim 3, wherein said modified amino acid is selected from the group consisting of a glycosylated amino acid, a methylated amino acid, a ribosylated amino acid, an isoprenylated amino acid, a lipid-linked amino acid, and an amino acid analog.
- 9. The method of claim 3, wherein said target motif is selected from the group consisting of a single phosphothreonine, a single phosphosprine, and a single phosphotyrosine.
- 10. The method of claim 3, wherein said target motif consists of a single acetyl-lysine or a single nitrotyrosine.



- 12. The method of claim 11, wherein said kinase consensus substrate motif is selected from the group consisting of a MAPK consensus substrate motif, a CDK consensus substrate motif, a PKA consensus substrate motif, an Akt consensus substrate motif, a PKC consensus substrate motif, and an ATM consensus substrate motif, and wherein said protein binding motif is selected from the group consisting of a 14-3-3 consensus binding motifs, and a PDK1/bulky-ring consensus docking motif.
- 13. The method of claim 11, wherein said kinase consensus substrate motif is selected from the group consisting of a PKC Zeta consensus substrate motif, an ABL kinase consensus substrate motif, a CDK5 consensus substrate motif, an insulin receptor consensus substrate motif, a CaMKII consensus substrate motifs, a Src kinase consensus substrate motifs, a CDC2/CDK2 consensus substrate motifs, and a GSK3 kinase consensus substrate motifs, and wherein said protein binding motif is a PI3K P85 consensus binding motif.
- 14. The method of claim 3, wherein said target motif is phosphothreonine-X-(R/K) or proline-phosphoserine-proline.
- 15. The method of claim 1 or 3, wherein said peptide library is from 6 to 20 amino acids long.
- 16. The method of claim 1 or 3, wherein said peptide library is from 6 to 14 amino acids long.



- 17. A method for producing a motif-specific, context-independent antibody that recognizes a plurality of peptides or proteins within a genome that contain the motif, said method comprising the steps of:
 - (a) constructing a degenerate peptide library comprising (i) afixed target motif comprising one to six invariant amino acids, and(ii) a plurality of degenerate amino acids flanking said motif;
 - (b) immunizing a host with said peptide library to raise a context-independent antibody specific for a motif consisting of all or part of said target motif; and
 - (c) isolating antisera from said host, and purifying the motifspecific, context-independent antibody of step (b) from said antisera, said antibody recognizing a plurality of peptides or proteins within a genome that contain said motif.
- 18. A method for producing a motif-specific, context-independent antibody that recognizes a plurality of peptides or proteins within a genome that contain the motif, said method comprising the steps of:
 - (a) constructing a degenerate peptide library comprising (i) a fixed target motif comprising one to six invariant amino acids including at least one modified amino acid, and (ii) a plurality of degenerate amino acids flanking said motif, wherein said peptide library is from 6 to 20 amino acids long;
 - (b) immunizing a host with said peptide library to raise a context-independent antibody specific for a motif consisting of all or part of said target motif; and
 - (c) isolating antisera from said host, and purifying the motifspecific, context-independent antibody of step (b) from said antisera, said antibody recognizing a plurality of peptides or proteins within a genome that contain said motif.

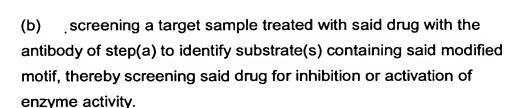
- 19. A motif-specific, context-independent antibody produced by the method of any one of claims 1-3 and 17-18.
- 20. A motif-specific, context-independent antibody which recognizes a plurality of peptides or proteins within a genome that contain said motif, wherein said motif comprises one to six invariant amino acids.
- 21. A motif-specific, context-independent antibody which recognizes a plurality of peptides or proteins within a genome that contain said motif, wherein said motif comprises one to six invariant amino acids including at least one modified amino acid.
- 22. The antibody of claim 21, wherein said motif is selected from the group consisting of a single phosphothreonine, a single phosphotyrosine, a single phosphotyrosine, a single acetyl-lysine, and a single nitrotyrosine.
- 23. The antibody of claim 22, wherein said motif comprises all or part of a kinase consensus substrate motif or a protein binding motif.
- 24. The antibody of claim 23, wherein said kinase substrate motif is selected from the group consisting of a MAPK consensus substrate motif, a CDK consensus substrate motif, a PKA consensus substrate motif, an Akt consensus substrate motif, a PKC consensus substrate motifs, and an ATM consensus substrate motifs, and wherein said protein binding motif is selected from the group consisting of a 14-3-3 consensus binding motif, and a PDK1/bulky-ring consensus docking motif.
- 25. The antibody of claim 23, wherein said kinase consensus substrate motif is selected from the group consisting of a PKC Zeta consensus substrate motif, an ABL kinase consensus substrate motif, a CDK5 consensus substrate motif, an insulin receptor consensus substrate motif, a CaMKII consensus substrate motif, a Src kinase

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consensus substrate motif, a CDC2/CDK2 consensus substrate motif, and a GSK3 kinase consensus substrate motif, and wherein said protein binding motif is a PI3K P85 consensus binding motif.

- 26. The antibody of claim 21, wherein said motif is phosphothreonine-X-(R/K) or proline-(phosphoserine/phosphothreonine)-proline.
- **27**. A method for identifying an unknown substrate of an enzyme, said method comprising the steps of:
 - generating at least one motif-specific, context-independent (a) antibody which recognizes a motif common to a plurality of substrates of said enyzme within a genome; and
 - screening a target sample with the antibody of step(a) to (b) identify an unknown substrate containing said motif.
- 28. A method for detecting the modification state of a target substrate that contains a motif common to a plurality of substrates of an enzyme within a genome, said method comprising the steps of:
 - generating at least one motif-specific, context-independent (a) antibody which recognizes the modified form of said motif; and
 - screening a target sample with the antibody of step(a) for (b) the presence of target substrate containing said modified motif, thereby detecting the modification state of said substrate.
- 29. A method for screening a drug for the inhibition or activation of enzyme activity on at least one substrate that contains a motif common to a plurality of substrates of said enyzme within a genome, said method comprising the steps of:
 - generating at least one motif-specific, context-independent (a) antibody which recognizes the modified form of said motif; and



- 30. A method for identifying an enzyme which modifies a known substrate that contains a motif common to a plurality of substrates of said enzyme within a genome, said method comprising the steps of:
 - (a) generating at least one motif-specific, context-independent antibody which recognizes the modified form of said motif;
 - (b) reacting an enzyme sample with a known substrate comprising the unmodified form of said motif; and
 - (c) screening with said antibody of step (a) for the presence of modified substrate resulting from step(b), thereby identifying if said enzyme modifies said known substrate.
- 31. A method for profiling protein levels or post-translational modifications in a cell or tissue on a genome wide scale, said method comprising the steps of:
 - (a) generating at least one motif-specific, context-independent antibody which recognizes the modified form of a motif common to a plurality of proteins within a genome;
 - (b) preparing an extract of a cell or tissue; and
 - (c) utilizing said antibody of step (a) to detect one or more proteins in the extract of step (b) that contain said modified motif, thereby profiling protein levels or post-translational modifications in said cell or tissue on a genome-wide scale.
- 32. A method for profiling drug-induced changes in protein levels or post-translational modifications in a cell or tissue on a genome wide scale, said method comprising the steps of:

- (a) generating at least one motif-specific, context-independent antibody which recognizes the modified form of a motif common to a plurality of different proteins within a genome;
- (b) preparing an extract of a cell or tissue treated with said drug; and
- (c) utilizing said antibody of step (a) to profile drug-induced changes in the level or post-translational modification of one or more proteins containing said modified motif present in the extract of step (b) as compared against an untreated control extract.
- 33. The method of any one of claims 27-32, wherein said motif is selected from the group consisting of a single phosphothreonine, a single phosphoterine, a single phosphotyrosine, a single acetyl-lysine, and a single nitrotyrosine.
- 34. The method of any one of claims 27-32, wherein said motif comprises all or part of a kinase consensus substrate motif or a protein binding motif.
- 35. The method of any one of claims 27-32, wherein said motif is selected from the group consisting of all or part of a MAPK consensus substrate motif, a CDK consensus substrate motif, a PKA consensus substrate motif, an Akt consensus substrate motif, a PKC consensus substrate motif, an ATM consensus substrate motif, a 14-3-3 consensus binding motif, a PDK1/bulky-ring consensus docking motif, and phosphothreonine-X-(R/K).
- 36. The method of any one of claims 27-32, wherein said motif is selected from the group consisting of all or part of a PKC Zeta consensus substrate motif, a ABL kinase consensus substrate motif, a CDK5 consensus substrate motif, an insulin receptor consensus substrate motif,

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a CaMKII consensus substrate motif, a Src kinase consensus substrate motif, a CDC2/CDK2 consensus substrate motif, a GSK3 kinase consensus substrate motif, a PI3K P85 consensus binding motif, and proline-phosphoserine-proline.

- 37. A motif-specific, context-independent antibody which recognizes a plurality of peptides or proteins within a genome that contain said motif, wherein said motif comprises two to six invariant amino acids including at least one phosphotyrosine.
- 38. A motif-specific, context-independent antibody which recognizes a plurality of peptides or proteins within a genome that contain said motif, wherein said motif comprises one to six invariant amino acids including at least one phosphoserine but does not consist of phosphoserine-proline.
- 39. A motif-specific, context-independent antibody which recognizes a plurality of peptides or proteins within a genome that contain said motif, wherein said motif comprises two to six invariant amino acids including at least one phosphothreonine.
- 40. The antibody of any one of claims 37-39, wherein said motif comprises all or part of a kinase consensus substrate motif or a protein binding motif.
- 41. A motif-specific, context-independent antibody which recognizes a plurality of peptides or proteins within a genome that contain said motif, wherein said motif consists of a single phosphothreonine, and wherein the specificity of said antibody is independent of variations in the amino acid residue at the -1 position relative to said motif, as determined by peptide grid analysis.



- 42. A motif-specific, context-independent antibody which recognizes a plurality of peptides or proteins within a genome that contain said motif, wherein said motif is selected from the group consisting of all or part of an MAPK consensus substrate motif, a CDK consensus substrate motif, and a 14-3-3 consensus binding motif.
- 43. A motif-specific, context-independent antibody which recognizes a plurality of peptides or proteins within a genome that contain said motif, wherein said motif is selected from the group consisting of all or part of an Akt consensus substrate motif, a PKA consensus substrate motif, and a bulky-ring/PDK1 consensus docking motif.
- 44. A motif-specific, context-independent antibody which recognizes a plurality of peptides or proteins within a genome that contain said motif, wherein said motif is selected from the group consisting of all or part of a PKC consensus substrate motif or an ATM consensus substrate motif, and phosphothreonine-X-(R/K).
- 45. A motif-specific, context-independent antibody which recognizes a plurality of peptides or proteins within a genome that contain said motif, wherein said motif is selected from the group consisting of all or part of a PKC Zeta consensus substrate motif, an ABL consensus substrate motif, a CDK5 consensus substrate motif, an insulin receptor consensus substrate motif, a PI3K P85 consensus binding motif, a CaMKII consensus substrate motif, a Src kinase consensus substrate motif, a CDC2/CDK2 consensus substrate motif, a GSK3 kinase consensus substrate motif, and proline-(phosphoserine/phosphothreonine)-proline.